

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/628,126DATE: 10/05/2000  
TIME: 01:21:25

INPUT SET: S35970.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Goodwin, Raymond G.  
Smith, Craig A.  
Armitage, Richard J.  
Gruss, Hans-Jurgen

(ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30

(iii) NUMBER OF SEQUENCES: 23

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
(B) STREET: 51 University Street  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98101

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Apple 7.1  
(D) SOFTWARE: Microsoft Word, Version 5.1a

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/628,126  
(B) FILING DATE: 28-JULY-2000  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/570,923  
(B) FILING DATE: 12-DEC-1995  
(A) APPLICATION NUMBER: US/08/225,989  
(B) FILING DATE: 12 APRIL 1994  
(A) APPLICATION NUMBER: US 07/966,775  
(B) FILING DATE: 27-OCT-1992  
(A) APPLICATION NUMBER: US 907,224  
(B) FILING DATE: 01-JUL-1992  
(A) APPLICATION NUMBER: US 899,660  
(B) FILING DATE: 15-JUN-1992  
(A) APPLICATION NUMBER: US 892,459  
(B) FILING DATE: 02-JUN-1992  
(A) APPLICATION NUMBER: US 889,717

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/628,126DATE: 10/05/2000  
TIME: 01:21:26

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47 (B) FILING DATE: 26-MAY-1992  
48  
49 (viii) ATTORNEY/AGENT INFORMATION:  
50 (A) NAME: Seese, Kathryn A.  
51 (B) REGISTRATION NUMBER: 32,172  
52 (C) REFERENCE/DOCKET NUMBER: 2804-E  
53  
54 (ix) TELECOMMUNICATION INFORMATION:  
55 (A) TELEPHONE: (206)587-0430  
56 (B) TELEFAX: (206)233-0644  
57 (C) TELEX: 756822  
58  
59  
60 (2) INFORMATION FOR SEQ ID NO:1:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 1788 base pairs  
64 (B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single  
66 (D) TOPOLOGY: linear  
67  
68 (ii) MOLECULE TYPE: cDNA to mRNA  
69  
70 (iii) HYPOTHETICAL: NO  
71  
72 (iv) ANTI-SENSE: NO  
73  
74  
75 (vii) IMMEDIATE SOURCE:  
76 (B) CLONE: huCD30  
77  
78 (ix) FEATURE:  
79 (A) NAME/KEY: CDS  
80 (B) LOCATION: 1..1788  
81  
82  
83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
84  
85 ATG CGC GTC CTC CTC GCC GCG CTG GGA CTG CTG TTC CTG GGG GCG CTA 48  
86 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu  
87 1 5 10 15  
88  
89 CGA GCC TTC CCA CAG GAT CGA CCC TTC GAG GAC ACC TGT CAT GGA AAC 96  
90 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn  
91 20 25 30  
92  
93 CCC AGC CAC TAC TAT GAC AAG GCT GTC AGG AGG TGC TGT TAC CGC TGC 144  
94 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys  
95 35 40 45  
96  
97 CCC ATG GGG CTG TTC CCG ACA CAG CAG TGC CCA CAG AGG CCT ACT GAC 192  
98 Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp  
99 50 55 60

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100																		
101	TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC	240	
102	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg		
103	65					70					75					80		
104																		
105	TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG	288	
106	Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr		
107					85					90					95			
108																		
109	CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG	336	
110	Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met		
111				100					105					110				
112																		
113	TTC	TGT	TCC	ACG	TCT	GCC	GTC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT	384	
114	Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His		
115			115					120					125					
116																		
117	TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG	432	
118	Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln		
119		130					135					140						
120																		
121	AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT	480	
122	Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys		
123	145					150					155					160		
124																		
125	GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG	528	
126	Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln		
127					165					170					175			
128																		
129	GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG	576	
130	Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met		
131				180					185					190				
132																		
133	CCT	GTA	AGA	GGG	GGC	ACC	CGC	CTC	GCC	CAG	GAA	GCT	GCT	TCT	AAA	CTG	624	
134	Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu		
135			195					200					205					
136																		
137	ACG	AGG	GCT	CCC	GAC	TCT	CCC	TCC	TCT	GTG	GGA	AGG	CCT	AGT	TCA	GAT	672	
138	Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp		
139		210					215											

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153	TGT	GCA	TGG	AAC	TCC	TCC	CGC	ACC	TGC	GAA	TGT	CGA	CCT	GGC	ATG	ATC	864
154	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	
155			275					280					285				
156																	
157	TGT	GCC	ACA	TCA	GCC	ACC	AAC	TCC	TGT	GCC	CGC	TGT	GTC	CCC	TAC	CCA	912
158	Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	
159		290					295						300				
160																	
161	ATC	TGT	GCA	GGA	GAG	ACG	GTC	ACC	AAG	CCC	CAG	GAT	ATG	GCT	GAG	AAG	960
162	Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	
163	305					310					315					320	
164																	
165	GAC	ACC	ACC	TTT	GAG	GCG	CCA	CCC	CTG	GGG	ACC	CAG	CCG	GAC	TGC	AAC	1008
166	Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	
167				325						330					335		
168																	
169	CCC	ACC	CCA	GAG	AAT	GGC	GAG	GCG	CCT	GCC	AGC	ACC	AGC	CCC	ACT	CAG	1056
170	Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	
171			340						345					350			
172																	
173	AGC	TTG	CTG	GTG	GAC	TCC	CAG	GCC	AGT	AAG	ACG	CTG	CCC	ATC	CCA	ACC	1104
174	Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	
175		355					360						365				
176																	
177	AGC	GCT	CCC	GTC	GCT	CTC	TCC	TCC	ACG	GGG	AAG	CCC	GTT	CTG	GAT	GCA	1152
178	Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala	
179		370				375						380					
180																	
181	GGG	CCA	GTG	CTC	TTC	TGG	GTG	ATC	CTG	GTG	TTG	GTT	GTG	GTG	GTC	GGC	1200
182	Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly	
183	385					390					395					400	
184																	
185	TCC	AGC	GCC	TTC	CTC	CTG	TGC	CAC	CGG	AGG	GCC	TGC	AGG	AAG	CGA	ATT	1248
186	Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile	
187				405					410					415			
188																	
189	CGG	CAG	AAG	CTC	CAC	CTG	TGC	TAC	CCG	GTC	CAG	ACC	TCC	CAG	CCC	AAG	1296
190	Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys	
191			420					425					430				
192																	
193	CTA	GAG	CTT	GTG	GAT	TCC	AGA	CCC	AGG	AGG	AGC	TCA	ACG	CAG	CTG	AGG	1344
194	Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg	
195		435					440					445					
196																	
197	AGT	GGT	GCG	TCG	GTG	ACA	GAA	CCC	GTC	GCG	GAA	GAG	CGA	GGG	TTA	ATG	1392
198	Ser	Gly	Ala	Ser	Val	Thr	Glu	Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met	
199		450				455					460						
200																	
201	AGC	CAG	CCA	CTG	ATG	GAG	ACC	TGC	CAC	AGC	GTG	GGG	GCA	GCC	TAC	CTG	1440
202	Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu	
203	465					470					475				480		
204																	
205	GAG	AGC	CTG	CCG	CTG	CAG	GAT	GCC	AGC	CCG	GCC	GGG	GGC	CCC	TCG	TCC	1488

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206  Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
207              485                      490                      495
208
209  CCC AGG GAC CTT CCT GAG CCC CGG GTG TCC ACG GAG CAC ACC AAT AAC 1536
210  Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
211              500                      505                      510
212
213  AAG ATT GAG AAA ATC TAC ATC ATG AAG GCT GAC ACC GTG ATC GTG GGG 1584
214  Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
215              515                      520                      525
216
217  ACC GTG AAG GCT GAG CTG CCG GAG GGC CGG GGC CTG GCG GGG CCA GCA 1632
218  Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
219              530                      535                      540
220
221  GAG CCC GAG TTG GAG GAG GAG CTG GAG GCG GAC CAT ACC CCC CAC TAC 1680
222  Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
223  545                      550                      555                      560
224
225  CCC GAG CAG GAG ACA GAA CCG CCT CTG GGC AGC TGC AGC GAT GTC ATG 1728
226  Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
227              565                      570                      575
228
229  CTC TCA GTG GAA GAG GAA GGG AAA GAA GAC CCC TTG CCC ACA GCT GCC 1776
230  Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
231              580                      585                      590
232
233  TCT GGA AAG TGA                      1788
234  Ser Gly Lys
235              595
236
237
238  (2) INFORMATION FOR SEQ ID NO:2:
239
240      (i) SEQUENCE CHARACTERISTICS:
241          (A) LENGTH: 595 amino acids
242          (B) TYPE: amino acid
243          (D) TOPOLOGY: linear
244
245      (ii) MOLECULE TYPE: protein
246
247      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
248
249  Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
250      1                      5                      10                      15
251

```

252 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn  
253 20 25 30  
254  
255 Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys  
256 35 40 45  
257  
258 Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/628,126**

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Line

Error

Original Text